IN THE CLAIMS:

Claims 1, 2, 3, 20, 21, 22, 39, 40, and 41 have been amended. Claims 1-4, 9, 12, 15, 20-23, 28, 31, 34, 39-42, 47, 50, and 58-73 are pending in the present application. The following is the status of the claims of the above-captioned application, as amended.

1. (Currently Amended) A method of producing a heterologous ~~biological substance~~ protein, comprising:

(a) cultivating a mutant of a parent *Bacillus* cell in a medium suitable for the production of the heterologous ~~biological substance~~ protein, wherein the mutant cell comprises a first nucleic acid sequence encoding ~~a~~ the heterologous protein~~, wherein the heterologous protein is the heterologous biological substance or the heterologous protein is involved in the synthesis of the heterologous biological substance,~~ and a second nucleic acid sequence comprising a mutation of at least one of the genes *cypX* and *yvmC*, wherein the mutation renders the mutant cell deficient in the production of ~~the~~ a red pigment compared to the parent *Bacillus* cell when cultivated under the same conditions, wherein the *cypX* gene comprises the nucleic acid sequence of SEQ ID NO: 1 or comprises a nucleic acid sequence having at least 70% homology to SEQ ID NO: 1, and the *yvmC* gene comprises the nucleic acid sequence of SEQ ID NO: ~~3~~ 7 or comprises a nucleic acid sequence having at least 70% homology to SEQ ID NO: ~~3~~ 7; and

(b) recovering the heterologous ~~biological substance~~ protein from the cultivation medium.

2. (Currently Amended) The method of claim 1, wherein at least one gene of the second nucleic acid sequence is *cypX* comprising the nucleic acid sequence of SEQ ID NO: 1 or a nucleic acid sequence having at least 70% homology to SEQ ID NO: 1.

3. (Currently Amended) The method of claim 1, wherein at least one gene of the second nucleic acid sequence is *yvmC* comprising the nucleic acid sequence of SEQ ID NO: 7 or a nucleic acid sequence having at least 70% homology to SEQ ID NO: 7.

4. (Previously Presented) The method of claim 1, wherein the heterologous protein encoded by the first nucleic acid sequence is involved in the biosynthesis of a biopolymer.

5-8. (Canceled).

9. (Previously Presented) The method of claim 1, wherein the heterologous protein encoded by the first nucleic acid sequence is involved in the biosynthesis of a metabolite.

10. (Canceled).

11. (Canceled).

12. (Original) The method of claim 1, wherein the *Bacillus* cell is a *Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus brevis, Bacillus circulans, Bacillus clausii, Bacillus coagulans, Bacillus firmus, Bacillus lautus, Bacillus lentus, Bacillus licheniformis, Bacillus megaterium, Bacillus pumilus, Bacillus stearothermophilus, Bacillus subtilis,* or *Bacillus thuringiensis* cell.

13-14. (Canceled).

15. (Original) The method of claim 1, wherein the mutant cell produces at least about 25% less of the red pigment compared to the parent *Bacillus* cell when cultured under identical conditions.

16-19. (Canceled).

20. (Currently Amended) A mutant of a parent *Bacillus* cell for producing a heterologous ~~biological substance~~ protein, comprising a first nucleic acid sequence encoding ~~a~~ the heterologous protein~~, wherein the heterologous protein is the heterologous biological substance or the heterologous protein is involved in the synthesis of the heterologous biological substance,~~ and a second nucleic acid sequence comprising mutation of at least one of the genes *cypX* and *yvmC*, wherein the mutation renders the mutant cell deficient in the production of the red pigment compared to the parent *Bacillus* cell when cultivated under the same conditions and wherein the *cypX* gene comprises the nucleic acid sequence of SEQ ID NO: 1 or comprises a nucleic acid sequence having at least 70% homology to SEQ ID NO: 1, and the

yvmC gene comprises the nucleic acid sequence of SEQ ID NO: 7 or comprises a nucleic acid sequence having at least 70% homology to SEQ ID NO: 7.

21. (Currently Amended) The mutant cell of claim 20, wherein at least one gene of the second nucleic acid sequence is *cypX* comprising the nucleic acid sequence of SEQ ID NO: 1 or a nucleic acid sequence having at least 70% homology to SEQ ID NO: 1.

22. (Currently Amended) The mutant cell of claim 20, wherein at least one gene of the second nucleic acid sequence is *yvmC* comprising the nucleic acid sequence of SEQ ID NO: 7 or a nucleic acid sequence having at least 70% homology to SEQ ID NO: 7.

23. (Previously Presented) The mutant cell of claim 20, wherein the heterologous protein encoded by the first nucleic acid sequence is involved in the biosynthesis of a biopolymer.

24-27. (Canceled).

28. (Previously Presented) The mutant cell of claim 20, wherein the heterologous protein encoded by the first nucleic acid sequence is involved in the biosynthesis of a metabolite.

29-30. (Canceled).

31. (Original) The mutant cell of claim 20, wherein the *Bacillus* cell is a *Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus brevis, Bacillus circulans, Bacillus clausii, Bacillus coagulans, Bacillus firmus, Bacillus lautus, Bacillus lentus, Bacillus licheniformis, Bacillus megaterium, Bacillus pumilus, Bacillus stearothermophilus, Bacillus subtilis,* or *Bacillus thuringiensis* cell.

32-33. (Canceled).

34. (Original) The mutant cell of claim 20, which produces at least about 25% less of the red pigment compared to the parent *Bacillus* cell when cultured under identical conditions.

35-38. (Canceled).

39. (Currently Amended) A method of ~~obtaining~~ isolating a mutant of a parent *Bacillus* cell, comprising:

(a) introducing into the parent *Bacillus* cell a first nucleic acid sequence directing synthesis of a heterologous ~~biological substance~~ protein and a second nucleic acid sequence comprising a mutation of at least one of the genes *cypX* and *yvmC*, wherein the mutation renders the mutant cell deficient in the production of a red pigment compared to the parent *Bacillus* cell when cultivated under the same conditions, and wherein the *cypX* gene comprises the nucleic acid sequence of SEQ ID NO: 1 or comprises a nucleic acid sequence having at least 70% homology to SEQ ID NO: 1, and the *yvmC* gene comprises the nucleic acid sequence of SEQ ID NO: ~~3~~ 7 or comprises a nucleic acid sequence having at least 70% homology to SEQ ID NO: ~~3~~ 7; and

(b) ~~identifying~~ isolating the mutant cell from step (a) comprising the mutation of at least one of the genes *cypX* and *yvmC*.

40. (Currently Amended) The method of claim 39, wherein at least one gene of the second nucleic acid sequence is *cypX* comprising the nucleic acid sequence of SEQ ID NO: 1 or a nucleic acid sequence having at least 70% homology to SEQ ID NO: 1.

41. (Currently Amended) The method of claim 39, wherein at least one gene of the second nucleic acid sequence is *yvmC* comprising the nucleic acid sequence of SEQ ID NO: 7 or a nucleic acid sequence having at least 70% homology to SEQ ID NO: 7.

42. (Previously Presented) The method of claim 39, wherein the heterologous protein encoded by the first nucleic acid sequence is involved in the biosynthesis of a biopolymer.

43-46. (Canceled).

47. (Previously Presented) The method of claim 39, wherein the heterologous protein encoded by the first nucleic acid sequence is involved in the biosynthesis of a metabolite.

48-49. (Canceled).

50. (Original) The method of claim 39, wherein the *Bacillus* cell is a *Bacillus alkalophilus, Bacillus amyloliquefaciens, Bacillus brevis, Bacillus circulans, Bacillus clausii, Bacillus coagulans, Bacillus firmus, Bacillus lautus, Bacillus lentus, Bacillus licheniformis, Bacillus megaterium, Bacillus pumilus, Bacillus stearothermophilus, Bacillus subtilis,* or *Bacillus thuringiensis* cell.

51-57. (Cancelled).

58. (New) The method of claim 1, wherein the *Bacillus* cell is a *Bacillus subtilis* cell.

59. (New) The method of claim 1, wherein the *Bacillus* cell is a *Bacillus licheniformis* cell.

60. (New) The method of claim 1, wherein the mutant cell further comprises a mutation of one or more genes which encode a protease.

61. (New) The method of claim 60, wherein the genes are *nprE* and/or *aprE*.

62. (New) The method of claim 1, wherein the mutant cell further comprises a modification of one or more genes selected from the group consisting of *spoIIAC*, *srfA*, *srfB*, *srfC*, *srfD*, and *amyE* genes.

63. (New) The mutant cell of claim 20, which is a *Bacillus subtilis* cell.

64. (New) The mutant cell of claim 20, which is a *Bacillus licheniformis* cell.

65. (New) The mutant cell of claim 20, which further comprises a mutation of one or more genes which encode a protease.

66. (New) The mutant cell of claim 65, wherein the genes are *nprE* and/or *aprE*.

67. (New) The mutant cell of claim 20, which further comprises a modification of one or more genes selected from the group consisting of *spoIIAC*, *srfA*, *srfB*, *srfC*, *srfD*, and *amyE* genes.

68. (New) The method of claim 39, wherein the *Bacillus* cell is a *Bacillus subtilis* cell.

69. (New) The method of claim 39, wherein the *Bacillus* cell is a *Bacillus licheniformis* cell.

70. (New) The method of claim 39, wherein the mutant cell produces at least about 25% less of the red pigment than the parent *Bacillus* cell when cultured under identical conditions.

71. (New) The method of claim 39, wherein the mutant cell further comprises a mutation of one or more genes which encode a protease.

72. (New) The method of claim 71, wherein the genes are *nprE* and/or *aprE*.

73. (New) The method of claim 39, wherein the mutant cell further comprises a mutation of one or more genes selected from the group consisting of *spoIIAC*, *srfA*, *srfB*, *srfC*, *srfD*, and *amyE* genes.